

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 101595793  
Source: JHU  
Date Processed by STIC: 3/16/07

***ENTERED***



IFWO

**RAW SEQUENCE LISTING** DATE: 03/16/2007  
**PATENT APPLICATION:** US/10/595,793 TIME: 12:30:00

Input Set : N:\efs\03\_16\_07\10595793\_efs\101218\_Sequence\_List.txt  
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3 <110> APPLICANT: ASTRAZENECA AB  
4       Bostwick, Robert  
5       Corradi, John  
6       Defay, Thomas  
7       Furlong, Stephen  
8       Hirata, Lee T.  
9       Ravyn, Vipa  
10      Robbins, Alan  
12 <120> TITLE OF INVENTION: GNAL Splice Variant and Uses Thereof  
14 <130> FILE REFERENCE: 101218-1P US  
16 <140> CURRENT APPLICATION NUMBER: 10/595,793  
17 <141> CURRENT FILING DATE: 2006-05-11  
19 <150> PRIOR APPLICATION NUMBER: 60/519,190  
20 <151> PRIOR FILING DATE: 2003-11-11  
22 <150> PRIOR APPLICATION NUMBER: 60/607,010  
23 <151> PRIOR FILING DATE: 2004-09-03  
25 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/004749  
26 <151> PRIOR FILING DATE: 2004-11-11  
28 <160> NUMBER OF SEQ ID NOS: 45  
30 <170> SOFTWARE: PatentIn version 3.3  
32 <210> SEQ ID NO: 1  
33 <211> LENGTH: 1377  
34 <212> TYPE: DNA  
35 <213> ORGANISM: Homo sapiens  
37 <400> SEQUENCE: 1

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40 gccgcctcg	agccgcgg	ggaggacgc	cagccgc	cgccccccgg	cctggcccca	120
42 gtccggcg	ccgcaaggga	cacggcccgg	accctgctcc	ctcgccccgg	cgaaggggagc	180
44 ccggcatgc	ctcgccccaa	agcagacaag	ccgaaggaga	agcggcagcg	caccgagcag	240
46 ctgagtgc	aggagcgcga	ggcgccaaag	gagcgcgagg	cggtcaaggaa	ggcgaggaaa	300
48 gtgagccgg	gcatcgaccg	catgctgcgc	gaccagaagc	gcgacctgca	gcagacgcac	360
50 cggctcctgc	tgctcggggc	tggtagtct	ggaaaaagca	ctatcgtaa	acagatgagg	420
52 atcctgcacg	tcaatgggtt	taatcccgag	gaaaagaaac	agaaaattct	ggacatccgg	480
54 aaaaatgtta	aagatgttat	cgtgacaatt	gttccagcaa	tgagtactat	aatacctcca	540
56 gttccgctgg	ccaaccctga	aaaccaattt	cgatcagact	acatcaagag	catagccct	600
58 atcaactgact	ttgaatattc	ccaggaattt	tttgaccatg	tggaaaaact	ttgggacgat	660
60 gaaggcgtga	aggcatgctt	tgagagatcc	aacgaatacc	agctgattga	ctgtgcacaa	720
62 tactcctgg	aaagaatcga	cagcgtcagc	ttggttgact	acacacccac	agaccaggac	780
64 ctcctcagat	gcagagttct	gacatctggg	attttgaga	cacgattcca	agtggacaaa	840
66 gtaaaacttcc	acatgtttga	tgttgtggc	cagaggatg	agaggagaaa	atggatccag	900
68 tgcttaacg	atgtcacagc	tatcattac	gtcgccgcct	gcagtagcta	caacatggtg	960
70 attcgagaag	ataacaacac	caacaggctg	agagagtccc	ttggatcttt	tgaaaagcatc	1020
72 tggaaacaaca	ggtggttacg	gaccatttct	atcatcttgt	tcttgaacaa	acaagatatg	1080

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76	aattatactg	tccctgaaga	cgcacaccca	gatgcaggag	aagaccccaa	agttacaaga	1200										
78	gccaagttct	ttatccggga	cctgttttg	aggatcagca	cggccacccg	tgacggcaaa	1260										
80	cattactgct	acccgcactt	cacctgcgcc	gtggacacag	agaacatccg	cagggtgttc	1320										
82	aacgactgccc	gcgacatcat	ccagcggatg	cacctaagc	agtatgagct	cttgtga	1377										
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93	1				5					10				15			
96	Asp	Asp	Pro	Cys	Ala	Ala	Ser	Glu	Pro	Pro	Val	Glu	Asp	Ala	Gln	Pro	
97					20					25				30			
100	Ala	Pro	Ala	Pro	Ala	Leu	Ala	Pro	Val	Arg	Ala	Ala	Arg	Asp	Thr		
101						35			40				45				
104	Ala	Arg	Thr	Leu	Leu	Pro	Arg	Gly	Gly	Glu	Gly	Ser	Pro	Ala	Cys	Ala	
105						50			55				60				
108	Arg	Pro	Lys	Ala	Asp	Lys	Pro	Lys	Glu	Lys	Arg	Gln	Arg	Thr	Glu	Gln	
109	65					65			70				75			80	
112	Leu	Ser	Ala	Glu	Glu	Arg	Glu	Ala	Ala	Lys	Glu	Arg	Glu	Ala	Val	Lys	
113						85				90				95			
116	Glu	Ala	Arg	Lys	Val	Ser	Arg	Gly	Ile	Asp	Arg	Met	Leu	Arg	Asp	Gln	
117						100				105				110			
120	Lys	Arg	Asp	Leu	Gln	Gln	Thr	His	Arg	Leu	Leu	Leu	Gly	Ala	Gly		
121						115			120				125				
124	Glu	Ser	Gly	Lys	Ser	Thr	Ile	Val	Lys	Gln	Met	Arg	Ile	Leu	His	Val	
125						130			135				140				
128	Asn	Gly	Phe	Asn	Pro	Glu	Glu	Lys	Gln	Lys	Ile	Leu	Asp	Ile	Arg		
129	145					145			150				155			160	
132	Lys	Asn	Val	Lys	Asp	Ala	Ile	Val	Thr	Ile	Val	Ser	Ala	Met	Ser	Thr	
133						165				170				175			
136	Ile	Ile	Pro	Pro	Val	Pro	Leu	Ala	Asn	Pro	Glu	Asn	Gln	Phe	Arg	Ser	
137						180				185				190			
140	Asp	Tyr	Ile	Lys	Ser	Ile	Ala	Pro	Ile	Thr	Asp	Phe	Glu	Tyr	Ser	Gln	
141						195			200				205				
144	Glu	Phe	Phe	Asp	His	Val	Lys	Lys	Leu	Trp	Asp	Asp	Glu	Gly	Val	Lys	
145						210			215				220				
148	Ala	Cys	Phe	Glu	Arg	Ser	Asn	Glu	Tyr	Gln	Leu	Ile	Asp	Cys	Ala	Gln	
149	225					225			230				235			240	
152	Tyr	Phe	Leu	Glu	Arg	Ile	Asp	Ser	Val	Ser	Leu	Val	Asp	Tyr	Thr	Pro	
153						245				250				255			
156	Thr	Asp	Gln	Asp	Leu	Leu	Arg	Cys	Arg	Val	Leu	Thr	Ser	Gly	Ile	Phe	
157						260				265				270			
160	Glu	Thr	Arg	Phe	Gln	Val	Asp	Lys	Val	Asn	Phe	His	Met	Phe	Asp	Val	
161						275			280				285				
164	Gly	Gly	Gln	Arg	Asp	Glu	Arg	Arg	Lys	Trp	Ile	Gln	Cys	Phe	Asn	Asp	
165						290			295				300				
168	Val	Thr	Ala	Ile	Ile	Tyr	Val	Ala	Ala	Cys	Ser	Ser	Tyr	Asn	Met	Val	

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169	305	310	315	320
172	Ile Arg Glu Asp Asn Asn Thr Asn Arg Leu Arg Glu Ser Leu Asp Leu			
173	325	330	335	
176	Phe Glu Ser Ile Trp Asn Asn Arg Trp Leu Arg Thr Ile Ser Ile Ile			
177	340	345	350	
180	Leu Phe Leu Asn Lys Gln Asp Met Leu Ala Glu Lys Val Leu Ala Gly			
181	355	360	365	
184	Lys Ser Lys Ile Glu Asp Tyr Phe Pro Glu Tyr Ala Asn Tyr Thr Val			
185	370	375	380	
188	Pro Glu Asp Ala Thr Pro Asp Ala Gly Glu Asp Pro Lys Val Thr Arg			
189	385	390	395	400
192	Ala Lys Phe Phe Ile Arg Asp Leu Phe Leu Arg Ile Ser Thr Ala Thr			
193	405	410	415	
196	Gly Asp Gly Lys His Tyr Cys Tyr Pro His Phe Thr Cys Ala Val Asp			
197	420	425	430	
200	Thr Glu Asn Ile Arg Arg Val Phe Asn Asp Cys Arg Asp Ile Ile Gln			
201	435	440	445	
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205	450	455		
208	<210> SEQ ID NO: 3			
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218	gctaccacc gcctactgct cctggggct ggtgagtctg gaaaaagcac tatcgtcaaa	180		
220	cagatgagga tcctgcacgt caatgggtt aatcccggg aaaagaaaaca gaaaattctg	240		
222	gacatccgga aaaatgttaa agatgtatac gtgacaattt tttcagcaat gagtactata	300		
224	atacctccag ttccgcgtgc caaccctgaa aaccaatttc gatcagacta catcaagagc	360		
226	atagcccccta tcactgactt tgaatattcc caggaattct ttgaccatgt gaaaaaaactt	420		
228	tgggacgatg aaggcgtgaa ggcatgctt gagagatcca acgaatacca gctgattgac	480		
230	tgtgcacaat acttcctgga aagaatcgac agcgtcagct tggttgacta cacacccaca	540		
232	gaccaggacc tcctcagatg cagagttctg acatctgggaa tttttgagac acgattccaa	600		
234	gtggacaaag taaacctcca catgtttgat gttggtgcc agagggatga gaggagaaaa	660		
236	tggatccagt gcttaacgaa tgtcacagct atcatttacg tcgcagccctg cagtagctac	720		
238	aacatggta ttgcagaaga taacaacacc aacaggctga gagagtcctt ggtatctttt	780		
240	gaaagcatct ggaacaacag gtggttacgg accatttcta tcatcttgc ttttgcacaaa	840		
242	caagatatgc tggcagaaaa agtcttggca gggaaatcaa aaattgaaga ctatcccac	900		
244	gaatatgca attatactgt tcctgaagac gcaacaccag atgcaggaga agatccaaa	960		
246	gttacaagag ccaaggctt tatccggac ctgttttgc ggatcagcac ggcacccgg	1020		
248	gacggcaaac attactgcta cccgcacttc acctgcggcc tggacacacaga gaacatccgc	1080		
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260	<400> SEQUENCE: 4			

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263 1           5           10          15
266 Asp Glu Lys Glu Arg Arg Glu Ala Asn Lys Lys Ile Glu Lys Gln Leu
267 20          25          30
270 Gln Lys Glu Arg Leu Ala Tyr Lys Ala Thr His Arg Leu Leu Leu
271 35          40          45
274 Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln Met Arg Ile
275 50          55          60
278 Leu His Val Asn Gly Phe Asn Pro Glu Glu Lys Lys Gln Lys Ile Leu
279 65          70          75          80
282 Asp Ile Arg Lys Asn Val Lys Asp Ala Ile Val Thr Ile Val Ser Ala
283 85          90          95
286 Met Ser Thr Ile Ile Pro Pro Val Pro Leu Ala Asn Pro Glu Asn Gln
287 100         105         110
290 Phe Arg Ser Asp Tyr Ile Lys Ser Ile Ala Pro Ile Thr Asp Phe Glu
291 115         120         125
294 Tyr Ser Gln Glu Phe Phe Asp His Val Lys Lys Leu Trp Asp Asp Glu
295 130         135         140
298 Gly Val Lys Ala Cys Phe Glu Arg Ser Asn Glu Tyr Gln Leu Ile Asp
299 145         150         155         160
302 Cys Ala Gln Tyr Phe Leu Glu Arg Ile Asp Ser Val Ser Leu Val Asp
303 165         170         175
306 Tyr Thr Pro Thr Asp Gln Asp Leu Leu Arg Cys Arg Val Leu Thr Ser
307 180         185         190
310 Gly Ile Phe Glu Thr Arg Phe Gln Val Asp Lys Val Asn Phe His Met
311 195         200         205
314 Phe Asp Val Gly Gly Gln Arg Asp Glu Arg Arg Lys Trp Ile Gln Cys
315 210         215         220
318 Phe Asn Asp Val Thr Ala Ile Ile Tyr Val Ala Ala Cys Ser Ser Tyr
319 225         230         235         240
322 Asn Met Val Ile Arg Glu Asp Asn Asn Thr Asn Arg Leu Arg Glu Ser
323 245         250         255
326 Leu Asp Leu Phe Glu Ser Ile Trp Asn Asn Arg Trp Leu Arg Thr Ile
327 260         265         270
330 Ser Ile Ile Leu Phe Leu Asn Lys Gln Asp Met Leu Ala Glu Lys Val
331 275         280         285
334 Leu Ala Gly Lys Ser Lys Ile Glu Asp Tyr Phe Pro Glu Tyr Ala Asn
335 290         295         300
338 Tyr Thr Val Pro Glu Asp Ala Thr Pro Asp Ala Gly Glu Asp Pro Lys
339 305         310         315         320
342 Val Thr Arg Ala Lys Phe Phe Ile Arg Asp Leu Phe Leu Arg Ile Ser
343 325         330         335
346 Thr Ala Thr Gly Asp Gly Lys His Tyr Cys Tyr Pro His Phe Thr Cys
347 340         345         350
350 Ala Val Asp Thr Glu Asn Ile Arg Arg Val Phe Asn Asp Cys Arg Asp
351 355         360         365
354 Ile Ile Gln Arg Met His Leu Lys Gln Tyr Glu Leu Leu
355 370         375         380
358 <210> SEQ ID NO: 5

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/595,793

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